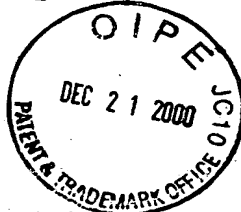


SEQUENCE LISTING



<110> Bermudes, G.  
King, I.  
Clairmont, C.  
Lin, S.  
Belcourt, M.

<120> COMPOSITIONS AND METHODS FOR  
TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES

<130> 8002-059

<150> 60/157,581

<151> 1999-10-04

<150> 60/157,637

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<220>

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26

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<400> 2

cgggatccga gctcgagggc ccgggaaagg atctaagaag atcc

44

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<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(474)

<400> 3

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Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His	
1 5 10 15	

gta gtt gct aac cct cag gca gaa ggt cag ctg cag tgg ctg aac cgt	96
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
20 25 30	

cgc gct aac gcc ctg ctg gca aac ggc gtt gag ctc cgt gat aac cag	144
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
35 40 45	

ctc gtg gta cct tct gaa ggt ctg tac ctg atc tat tct caa gta ctg	192
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	
50 55 60	

ttc aag ggt cag ggc tgc ccg tgc act cat gtt ctg ctg act cac acc	240
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr	
65 70 75 80	

atc agc cgt att gct gta tct tac cag acc aaa gtt aac ctg ctg agc	288
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	
85 90 95	

gct atc aag tct ccg tgc cag cgt gaa act ccc gag ggt gca gaa gcg	336
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	
100 105 110	

aaa cca tgg tat gaa ccg atc tac ctg ggt ggc gta ttt caa ctg gag	384
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu	
115 120 125	

aaa ggt gac cgt ctg tcc gca gaa atc aac cgt cct gac tat cta gat	432
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp	
130 135 140	

ttc gct gaa tct ggc cag gtg tac ttc ggt att atc gca ctg	474
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu	
145 150 155	

taa	477
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<210> 4  
 <211> 158  
 <212> PRT  
 <213> Homo sapiens

<400> 4	
Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His	
1 5 10 15	
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
20 25 30	
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
35 40 45	
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	
50 55 60	
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr	
65 70 75 80	

Ile	Ser	Arg	Ile	Ala	Val	Ser	Tyr	Gln	Thr	Lys	Val	Asn	Leu	Leu	Ser
				85					90					95	
Ala	Ile	Lys	Ser	Pro	Cys	Gln	Arg	Glu	Thr	Pro	Glu	Gly	Ala	Glu	Ala
			100					105					110		
Lys	Pro	Trp	Tyr	Glu	Pro	Ile	Tyr	Leu	Gly	Gly	Val	Phe	Gln	Leu	Glu
		115					120					125			
Lys	Gly	Asp	Arg	Leu	Ser	Ala	Glu	Ile	Asn	Arg	Pro	Asp	Tyr	Leu	Asp
	130					135					140				
Phe	Ala	Glu	Ser	Gly	Gln	Val	Tyr	Phe	Gly	Ile	Ile	Ala	Leu		
145					150					155					

<210> 5  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Forward primer

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<400> 5	
ccgacgcgtt gacacctgaa aactggag	28

<210> 6  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Reverse primer

<400> 6	
ccgacgcgtg aaaggatctc aagaagatc	29

<210> 7  
 <211> 543  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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<221> CDS  
 <222> (1)...(540)

<400> 7	
atg aaa aag aca gct atc gcg att gca gtg gca ctg gct ggt ttc gct	48
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala	
1 5 10 15	

acc gta gcg cag gcc cat atg gta cgt agc tcc tct cgc act ccg tcc	96
Thr Val Ala Gln Ala His Met Val Arg Ser Ser Ser Arg Thr Pro Ser	
20 25 30	

gat aag ccg gtt gct cat gta gtt gct aac cct cag gca gaa ggt cag	144
Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln	
35 40 45	

ctg cag tgg ctg aac cgt cgc gct aac gcc ctg ctg gca aac ggc gtt 192  
 Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val  
           50                                  55                                  60

gag ctg cgt gat aac cag ctg gtg gta cct tct gaa ggt ctg tac ctg 240  
 Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu  
           65                                  70                                  75                                  80

atc tat tct caa gta ctg ttc aag ggt cag ggc tgc ccg tct act cat 288  
 Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His  
                                   85                                  90                                  95

gtt ctg ctg act cac acc atc agc cgt att gct gta tct tac cag acc 336  
 Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr  
                                   100                                  105                                  110

aaa gtt aac ctg ctg agc gct atc aag tct ccg tgc cag cgt gaa act 384  
 Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr  
                                   115                                  120                                  125

ccc gag ggt gca gaa gcg aaa cca tgg tat gaa ccg atc tac ctg ggt 432  
 Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly  
           130                                  135                                  140

ggc gta ttt caa ctg gag aaa ggt gac cgt ctg tcc gca gaa atc aac 480  
 Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn  
           145                                  150                                  155                                  160

cgt cct gac tat cta gat ttc gct gaa tct ggc cag gtg tac ttc ggt 528  
 Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly  
                                   165                                  170                                  175

att atc gca ctg taa 543  
 Ile Ile Ala Leu  
                                   180

<210> 8  
 <211> 180  
 <212> PRT  
 <213> Artificial Sequence

<400> 8  
 Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala  
   1                  5                  10                  15  
 Thr Val Ala Gln Ala His Met Val Arg Ser Ser Ser Arg Thr Pro Ser  
           20                  25                  30  
 Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln  
           35                  40                  45  
 Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val  
   50                  55                  60  
 Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu  
   65                  70                  75                  80  
 Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His  
                   85                  90                  95  
 Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr  
           100                  105                  110

Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr  
           115                          120                          125  
 Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly  
           130                          135                          140  
 Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn  
 145                          150                          155                          160  
 Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly  
                           165                          170                          175  
 Ile Ile Ala Leu  
                           180

<210> 9  
 <211> 801  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Fusion construct

<221> CDS  
 <222> (1)...(798)

<400> 9  
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 Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala  
   1                          5                          10                          15  
  
 acc gta gcg cag gcc cat atg gct aac gag ctg aag cag atg cag gac 96  
 Thr Val Ala Gln Ala His Met Ala Asn Glu Leu Lys Gln Met Gln Asp  
                           20                          25                          30  
  
 aag tac tcc aaa agt ggc att gct tgt ttc tta aaa gaa gat gac agt 144  
 Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser  
                           35                          40                          45  
  
 tat tgg gac ccc aat gac gaa gag agt atg aac agc ccc tgc tgg caa 192  
 Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln  
                           50                          55                          60  
  
 gtc aag tgg caa ctc cgt cag ctc gtt aga aag atg att ttg aga acc 240  
 Val Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr  
   65                          70                          75                          80  
  
 tct gag gaa acc att tct aca gtt caa gaa aag caa caa aat att tct 288  
 Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser  
                           85                          90                          95  
  
 ccc cta gtg aga gaa aga ggt cct cag aga gta gca gct cac ata act 336  
 Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr  
                           100                          105                          110  
  
 ggg acc aga gga aga agc aac aca ttg tct tct cca aac tcc aag aat 384  
 Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn  
                           115                          120                          125  
  
 gaa aag gct ctg ggc cgc aaa ata aac tcc tgg gaa tca tca agg agt 432  
 Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser  
   130                          135                          140

ggg cat tca ttc ctg agc aac ttg cac ttg agg aat ggt gaa ctg gtc	480
Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val	
145 150 155 160	

atc cat gaa aaa ggg ttt tac tac atc tat tcc caa aca tac ttt cga	528
Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg	
165 170 175	

ttt cag gag gaa ata aaa gaa aac aca aag aac gac aaa caa atg gtc	576
Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val	
180 185 190	

caa tat att tac aaa tac aca agt tat cct gac cct ata ttg ttg atg	624
Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met	
195 200 205	

aaa agt gct aga aat agt tgt tgg tct aaa gat gca gaa tat gga ctc	672
Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu	
210 215 220	

tat tcc atc tat caa ggg gga ata ttt gag ctt aag gaa aat gac aga	720
Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg	
225 230 235 240	

att ttt gtt tct gta aca aat gag cac ttg ata gac atg gac cat gaa	768
Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu	
245 250 255	

gcc agt ttt ttc ggg gcc ttt tta gtt ggc taa	801
Ala Ser Phe Phe Gly Ala Phe Leu Val Gly	
260 265	

<210> 10

<211> 266

<212> PRT

<213> Artificial Sequence

<400> 10

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20 25 30	
Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser	
35 40 45	
Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln	
50 55 60	
Val Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr	
65 70 75 80	
Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser	
85 90 95	
Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr	
100 105 110	
Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn	
115 120 125	
Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser	
130 135 140	

Gly	His	Ser	Phe	Leu	Ser	Asn	Leu	His	Leu	Arg	Asn	Gly	Glu	Leu	Val
145					150					155					160
Ile	His	Glu	Lys	Gly	Phe	Tyr	Tyr	Ile	Tyr	Ser	Gln	Thr	Tyr	Phe	Arg
				165					170						175
Phe	Gln	Glu	Glu	Ile	Lys	Glu	Asn	Thr	Lys	Asn	Asp	Lys	Gln	Met	Val
			180					185					190		
Gln	Tyr	Ile	Tyr	Lys	Tyr	Thr	Ser	Tyr	Pro	Asp	Pro	Ile	Leu	Leu	Met
	195						200					205			
Lys	Ser	Ala	Arg	Asn	Ser	Cys	Trp	Ser	Lys	Asp	Ala	Glu	Tyr	Gly	Leu
	210				215					220					
Tyr	Ser	Ile	Tyr	Gln	Gly	Ile	Phe	Glu	Leu	Lys	Glu	Asn	Asp	Arg	
225				230					235					240	
Ile	Phe	Val	Ser	Val	Thr	Asn	Glu	His	Leu	Ile	Asp	Met	Asp	His	Glu
			245					250						255	
Ala	Ser	Phe	Phe	Gly	Ala	Phe	Leu	Val	Gly						
			260					265							

<210> 11

<211> 465

<212> DNA

<213> Artificial Sequence

<220>

<223> Fusion construct

<221> CDS

<222> (1)...(462)

<400> 11

atg	aaa	aag	acg	gct	ctg	gcg	ctt	ctg	ctc	ttg	ctg	tta	gcg	ctg	act	48
Met	Lys	Lys	Thr	Ala	Leu	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Leu	Thr	
1				5				10					15			
agt	gta	gcg	cag	gcc	gct	cct	act	agc	tcg	agc	act	aag	aaa	act	caa	96
Ser	Val	Ala	Gln	Ala	Ala	Pro	Thr	Ser	Ser	Ser	Thr	Lys	Lys	Thr	Gln	
			20					25					30			
ctg	caa	ttg	gag	cat	ctg	ctg	ctg	gat	ctg	cag	atg	att	ctg	aat	ggc	144
Leu	Gln	Leu	Glu	His	Leu	Leu	Leu	Asp	Leu	Gln	Met	Ile	Leu	Asn	Gly	
			35				40					45				
atc	aat	aac	tac	aag	aac	cct	aag	ctg	act	cgc	atg	ctg	act	ttc	aaa	192
Ile	Asn	Asn	Tyr	Lys	Asn	Pro	Lys	Leu	Thr	Arg	Met	Leu	Thr	Phe	Lys	
	50				55					60						
ttc	tac	atg	ccg	aaa	aag	gct	acc	gag	ctc	aaa	cat	ctc	cag	tgc	ctg	240
Phe	Tyr	Met	Pro	Lys	Lys	Ala	Thr	Glu	Leu	Lys	His	Leu	Gln	Cys	Leu	
	65				70				75					80		
gaa	gag	gaa	ctg	aag	ccg	ctg	gag	gaa	gta	ctt	aac	ctg	gca	cag	tct	288
Glu	Glu	Glu	Leu	Lys	Pro	Leu	Glu	Glu	Val	Leu	Asn	Leu	Ala	Gln	Ser	
				85					90					95		
aag	aac	ttc	cac	ctg	cgt	ccg	cgt	gac	ctg	atc	tcc	aac	atc	aat	gta	336
Lys	Asn	Phe	His	Leu	Arg	Pro	Arg	Asp	Leu	Ile	Ser	Asn	Ile	Asn	Val	
			100					105					110			

atc gtt ctt gag ctg aag gga tcc gaa acc acc ttc atg tgc gaa tac 384  
 Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr  
           115                          120                          125

gct gac gaa acc gcc acc att gtg gag ttc ctg aac cgt tgg atc acc 432  
 Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr  
           130                          135                          140

ttt gcc caa tcg atc att agc acg tta act taa 465  
 Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr  
 145                          150

<210> 12  
 <211> 154  
 <212> PRT  
 <213> Artificial Sequence

<400> 12  
 Met Lys Lys Thr Ala Leu Ala Leu Leu Leu Leu Leu Leu Ala Leu Thr  
   1                  5                  10                  15  
 Ser Val Ala Gln Ala Ala Pro Thr Ser Ser Thr Lys Lys Thr Gln  
                   20                  25                  30  
 Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly  
           35                  40                  45  
 Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys  
           50                  55                  60  
 Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu  
 65                  70                  75                  80  
 Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser  
                   85                  90                  95  
 Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val  
                   100                  105                  110  
 Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr  
           115                  120                  125  
 Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr  
           130                  135                  140  
 Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr  
 145                  150

<210> 13  
 <211> 465  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Fusion construct

<221> CDS  
 <222> (1)...(462)

<400> 13  
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 Met Lys Gln Ser Thr Leu Ala Leu Leu Leu Leu Leu Leu Ala Leu Thr  
   1                  5                  10                  15



agt gtg gcc aaa gcg gct cct act agc tcg agc act aag aaa act caa 96  
 Ser Val Ala Lys Ala Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln  
                   20                                  25                                  30

ctg caa ttg gag cat ctg ctg ctg gat ctg cag atg att ctg aat ggc 144  
 Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly  
                   35                                  40                                  45

atc aat aac tac aag aac cct aag ctg act cgc atg ctg act ttc aaa 192  
 Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys  
                   50                                  55                                  60

ttc tac atg ccg aaa aag gct acc gag ctc aaa cat ctc cag tgc ctg 240  
 Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu  
                   65                                  70                                  75                                  80

gaa gag gaa ctg aag ccg ctg gag gaa gta ctt aac ctg gca cag tct 288  
 Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser  
                                   85                                  90                                  95

aag aac ttc cac ctg cgt ccg cgt gac ctg atc tcc aac atc aat gta 336  
 Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val  
                                   100                                  105                                  110

atc gtt ctt gag ctg aag gga tcc gaa acc acc ttc atg tgc gaa tac 384  
 Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr  
                   115                                  120                                  125

gct gac gaa acc gcc acc att gtg gag ttc ctg aac cgt tgg atc acc 432  
 Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr  
                   130                                  135                                  140

ttt gcc caa tcg atc att agc acg tta act taa 465  
 Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr  
                   145                                  150

<210> 14  
 <211> 154  
 <212> PRT  
 <213> Artificial Sequence

<400> 14  
 Met Lys Gln Ser Thr Leu Ala Leu Leu Leu Leu Leu Leu Ala Leu Thr  
   1                                  5                                  10                                  15  
 Ser Val Ala Lys Ala Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln  
                   20                                  25                                  30  
 Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly  
                   35                                  40                                  45  
 Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys  
                   50                                  55                                  60  
 Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu  
   65                                  70                                  75                                  80  
 Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser  
                                   85                                  90                                  95  
 Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val  
                   100                                  105                                  110

Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr  
115 120 125  
Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr  
130 135 140  
Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr  
145 150

<210> 15  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Forward primer

<400> 15  
agtctagaca atcaggcgaa gaacgg 26

<210> 16  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Reverse primer

<400> 16  
agccatggag tcaccctcac ttttc 25

<210> 17  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Forward primer

<400> 17  
ggatccttaa gaccacttt cacatttaag t 31

<210> 18  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Reverse primer

<400> 18  
ggttccatgg ttcacttttc tctatcac 28

<210> 19  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Forward primer

<400> 19  
gtgtccatgg ggcacagcca ccgcgacttc cag 33

<210> 20  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Reverse primer

<400> 20  
acacgagctc ctacttgag gcagtcatga agct 34

<210> 21  
<211> 72  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Forward primer

<400> 21  
gtgtccatgg ctccggcgggc aagtgtcggg actgaccatc atcatcatca tcatcacagc 60  
caccgcgact tc 72

<210> 22  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Reverse primer

<400> 22  
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<212> PRT  
<213> Homo sapiens

<400> 23  
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<210> 24  
<211> 22  
<212> PRT  
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<220>  
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gaaggc 66

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<220>  
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35 40 45  
Gln Val Arg Pro Arg His Ile Thr Ser Leu Glu Val Ile Lys Ala Gly  
50 55 60  
Pro His Cys Pro Thr Ala Gln Leu Ile Ala Thr Leu Lys Asn Gly Arg  
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 50 55 60  
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37

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<211> 30

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<213> Artificial Sequence

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<223> Forward primer

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30

<210> 36

<211> 35

<212> DNA

<213> Artificial Sequence

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<223> Reverse primer

<400> 36

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35

<210> 37

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Forward primer

<400> 37

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<223> Reverse primer



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<400> 46  
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46

<210> 47  
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<220>  
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<400> 47  
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33

<210> 48  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 48  
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33

<210> 49

<211> 102  
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 <223> Oligonucleotide  


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<220>
<223> Oligonucleotide

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<210> 55
<211> 98
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

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<223> Oligonucleotide

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<210> 57
<211> 551
<212> DNA
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<220>
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<221> modified_base
<222> (1)...(1)
<223> n=a, c, g, or t

<400> 57
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1 5 10

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Asn Ala Leu Gln Glu Asp Thr Pro Pro Gly Pro Ser Thr Val Phe Arg
15 20 25 30

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ccg ccg acc tcc tcc cgc ccg ctg gaa acc ccg cat tgc cgc gaa atc	144
Pro Pro Thr Ser Ser Arg Pro Leu Glu Thr Pro His Cys Arg Glu Ile	
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cgc atc ggc atc gcg ggc atc acc atc acc ctg tcc ctg tgc ggc tgc	192
Arg Ile Gly Ile Ala Gly Ile Thr Ile Thr Leu Ser Leu Cys Gly Cys	
50 55 60	
gcg aac gcg cgc gcg ccg acc ctg cgc tcc gcg acc gcg gat aac tcc	240
Ala Asn Ala Arg Ala Pro Thr Leu Arg Ser Ala Thr Ala Asp Asn Ser	
65 70 75	
gaa aac acc ggc ttt aaa aac gtc ccg gat ctg cgc acc gat cag ccg	288
Glu Asn Thr Gly Phe Lys Asn Val Pro Asp Leu Arg Thr Asp Gln Pro	
80 85 90	
aaa ccg ccg tcc aaa aaa cgc tcc tgc gat ccg tcc gaa tat cgc gtc	336
Lys Pro Pro Ser Lys Lys Arg Ser Cys Asp Pro Ser Glu Tyr Arg Val	
95 100 105 110	
tcc gaa ctg aaa gaa tcc ctg atc acc acc acc ccg tcc cgc ccg cgc	384
Ser Glu Leu Lys Glu Ser Leu Ile Thr Thr Thr Pro Ser Arg Pro Arg	
115 120 125	
acc gcc cgc cgc tgc atc cgc ctc tgaaagcttg gctgttttgg cggatgagag	438
Thr Ala Arg Arg Cys Ile Arg Leu	
130	
aagatttttca gcctgataca gattaaatca gaacgcagaa gcggtctgat aaaacagaat	498
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<210> 58  
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 <212> PRT  
 <213> Bacteriophage

<400> 58	
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35 40 45	
Gly Ile Ala Gly Ile Thr Ile Thr Leu Ser Leu Cys Gly Cys Ala Asn	
50 55 60	
Ala Arg Ala Pro Thr Leu Arg Ser Ala Thr Ala Asp Asn Ser Glu Asn	
65 70 75 80	
Thr Gly Phe Lys Asn Val Pro Asp Leu Arg Thr Asp Gln Pro Lys Pro	
85 90 95	
Pro Ser Lys Lys Arg Ser Cys Asp Pro Ser Glu Tyr Arg Val Ser Glu	
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<210> 59  
 <211> 444

<212> DNA  
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<220>  
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<223> n=a, c, g, or t

<221> CDS  
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Arg Gln Arg Arg Arg Met Asn Ala Leu Gln Glu Asp Thr Pro Pro Gly  
15 20 25 30

ccg tcc acc gtg ttt cgc ccg ccg acc tcc tcc cgc ccg ctg gaa acc 144  
Pro Ser Thr Val Phe Arg Pro Pro Thr Ser Ser Arg Pro Leu Glu Thr  
35 40 45

ccg cat tgc cgc gaa atc cgc atc ggc atc gcg ggc atc acc atc acc 192  
Pro His Cys Arg Glu Ile Arg Ile Gly Ile Ala Gly Ile Thr Ile Thr  
50 55 60

ctg tcc ctg tgc ggc tgc gcg aac gcg cgc gcg ccg acc ctg cgc tcc 240  
Leu Ser Leu Cys Gly Cys Ala Asn Ala Arg Ala Pro Thr Leu Arg Ser  
65 70 75

gcg acc gcg gat aac tcc gaa aac acc ggc ttt aaa aac gtc ccg gat 288  
Ala Thr Ala Asp Asn Ser Glu Asn Thr Gly Phe Lys Asn Val Pro Asp  
80 85 90

ctg cgc acc gat cag ccg aaa ccg ccg tcc aaa aaa cgc tcc tgc gat 336  
Leu Arg Thr Asp Gln Pro Lys Pro Pro Ser Lys Lys Arg Ser Cys Asp  
95 100 105 110

ccg tcc gaa tat cgc gtc tcc gaa ctg aaa gaa tcc ctg atc acc acc 384  
Pro Ser Glu Tyr Arg Val Ser Glu Leu Lys Glu Ser Leu Ile Thr Thr  
115 120 125

acc ccg tcc cgc ccg cgc acc gcc cgc cgc tgc atc cgc ctc t 427  
Thr Pro Ser Arg Pro Arg Thr Ala Arg Arg Cys Ile Arg Leu  
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gaaagcttgg ctgtttt 444

<210> 60  
<211> 140  
<212> PRT  
<213> Bacteriophage

<400> 60  
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 Thr Val Phe Arg Pro Pro Thr Ser Arg Pro Leu Glu Thr Pro His  
 35 40 45  
 Cys Arg Glu Ile Arg Ile Gly Ile Ala Gly Ile Thr Ile Thr Leu Ser  
 50 55 60  
 Leu Cys Gly Cys Ala Asn Ala Arg Ala Pro Thr Leu Arg Ser Ala Thr  
 65 70 75 80  
 Ala Asp Asn Ser Glu Asn Thr Gly Phe Lys Asn Val Pro Asp Leu Arg  
 85 90 95  
 Thr Asp Gln Pro Lys Pro Pro Ser Lys Lys Arg Ser Cys Asp Pro Ser  
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 Glu Tyr Arg Val Ser Glu Leu Lys Glu Ser Leu Ile Thr Thr Thr Pro  
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<210> 61

<211> 1565

<212> DNA

<213> Salmonella

<400> 61

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gccggtgtta	atgcgatccc	cgccattgcc	gccgcgcca	accaggcgcc	ccaatactgt	1260
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